

Genomathematics

or the Science of Erased Trajectories

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Abstract

The approach presented here is part of a new epistemology: that of speculative but calculable sciences. Unlike classical science, which only describes and measures what exists, and unlike literary or philosophical speculation, which imagines without constraints of verification, these sciences aim to explore biological and evolutionary trajectories that are possible yet erased—hypothetical yet plausible—while relying on rigorous and reproducible methods.

Several earlier approaches paved the way without fully taking this step: information theory applied to the genome (Shannon, Kolmogorov), fractal and chaotic biology (Mandelbrot, Goodwin), or the speculations of exobiology (Crick, Sagan) on the universal laws of life. All highlighted the importance of mathematical patterns, but none proposed a systematic method for generating and testing alternative versions of life in a reproducible way.

This is precisely what the present approach allows: by applying systematic transformations of the genome ($A \leftrightarrow G$, $C \leftrightarrow T$ inversions), identifying multi-scale numerical invariants, or reconstructing phenotypes that never came to be through 3D modeling and bioinformatics, it becomes possible to formalize the study of virtual life. The results—whether expressed as arithmetic constants, mirror genomes recognized as plausible by databases, or faces derived from alternative evolutionary paths—do not stem from free imagination but from transparent and verifiable calculations.

In this sense, speculative but calculable sciences constitute a distinct domain: they do not merely document life as it is or was, but also map its erased potentialities—revealing invisible constraints, unrealized possibilities, and universal invariants underlying the logic of the living.

Their scope extends far beyond intellectual curiosity. These sciences open concrete perspectives in personalized medicine (through the modeling of virtual genetic twins), in augmented paleogenetics (exploring the erased trajectories of human evolution), in neuroscience (simulating alternative brain architectures), and in exobiology (offering universal criteria for life detection). They also hold direct relevance for synthetic biology: mirror genomes and numerical invariants provide a theoretical laboratory to test novel genetic architectures prior to experimental construction. Thus, speculative genomathematics provides a framework for anticipating the viability of artificial organisms, exploring

evolutionary paths never selected by nature, and expanding the repertoire of life forms created by humans.

At a time when biology is increasingly turning to artificial intelligence, modeling, and the fabrication of new organisms, it is essential to recognize this field as an autonomous discipline—not as a fringe of science, but as its natural extension into possible worlds.

Introduction – Towards a Science of Erased Trajectories

For more than a century, biology has been built on observation, experimentation, and the accumulation of data from the real world. It has described life in its diversity, measured variations in DNA, classified species, and reconstructed the evolutionary trajectories of those that once existed. Yet if science has been able to tell what *is*, and sometimes what *was*, it has rarely ventured into exploring what *could have been*: the erased trajectories of evolution, the possible but unrealized configurations of the living.

It is into this conceptual void that the present approach situates itself. It inaugurates a new epistemology: that of speculative but calculable sciences. Unlike literary or philosophical speculation, which imagines possible worlds without submitting them to verification, these sciences set themselves the task of exploring the virtual dimensions of life through rigorous, reproducible, and verifiable methods. Unlike classical science, which confines itself to what is observable, they allow themselves to question the shadow cast by evolution: what did not occur, but might have come to pass.

Legacies and Limits of Earlier Approaches

Several disciplines in the 20th century opened the way without fully taking this step.

- **Information theory applied to the genome (Shannon, Kolmogorov)** revealed that DNA can be read as a text subject to the laws of entropy and algorithmic complexity.
- **Fractal and chaotic biology (Mandelbrot, Goodwin)** showed that life obeys recurrent mathematical patterns, visible in organismal growth as well as in the organization of biological networks.
- **The tradition of natural forms governed by numbers** dates back to studies of phyllotaxis and the Fibonacci sequence (and its limiting ratio, ϕ , the “golden number”). From Kepler to D’Arcy Thompson, and later with modern models (the 34/55/89 spirals of floral capitula, pine cones, leaf arrangements), it has been shown that arithmetic and geometric laws govern plant morphogenesis. These regularities—further extended by Turing’s reaction–diffusion frameworks—established the legitimacy of mathematical motifs in biology. *Genomathematics* stands within this lineage while shifting the focus of analysis: from macroscopic forms to the informational level of the genome, where it seeks multi-scale numerical invariants and generates calculable alternative genomic trajectories (mirror genomes). This opens a field that no longer describes merely the order of forms, but the order of codes.

- **Speculative exobiology (Crick, Sagan)** suggested that certain structures of the genetic code might be universal, and therefore detectable beyond Earth.

These approaches highlighted the importance of mathematical structures in biology. But none has yet formulated a systematic method for generating, testing, and comparing alternative versions of life—that is, for putting into equations not only the real, but also its erased possibilities.

The Novelty of Genomathematics

This is precisely what *genomathematics*—the science of erased trajectories—proposes. This discipline emerges from a twofold observation:

- The genetic code can be conceived as a fractal mathematical object, governed by multi-level numerical invariants.
- The genome can be systematically transformed (through inversion, substitution, or calculable permutation) to generate plausible alternative versions, which can then be explored through bioinformatics, 3D modeling, and phenotypic reconstruction.

This approach has already given rise to three contributions:

1. **The identification of arithmetic invariants** within the structure of DNA, from elementary particles to codons, revealing an underlying mathematical grammar of life.
2. **The experimentation with the “mirror-twin paradox”**, which consists of systematically inverting nucleic bases ($A \leftrightarrow G$, $C \leftrightarrow T$) to generate an alternative genome, recognized as plausible by genetic databases.
3. **The development of a 3D reconstruction methodology** applied to inverted phenotypes, enabling the visualization of plausible but unrealized human faces and forms, and thus exploring the erased trajectories of human evolution.

These results do not stem from free imagination but from transparent and reproducible calculations, which can be repeated and verified by other researchers. They demonstrate that virtual life can be studied with the same rigor as real life.

A Distinct and Necessary Field

Genomathematics sets itself apart from existing disciplines:

- From **theoretical biology**, in that it does not confine itself to explanatory models but actively generates new calculable trajectories.
- From **bioinformatics**, in that it does not restrict itself to statistics on observed sequences, but ventures to create systematically transformed sequences.

- From **synthetic biology**, in that it does not directly construct new organisms, but explores a theoretical space of possibilities, serving as a virtual laboratory.

It therefore deserves to be recognized as an autonomous field—not as a fringe of science, but as its natural extension into possible worlds: those that evolution left behind, but which the human mind can resurrect through calculation.

Scope and Implications

The scope of such an approach extends far beyond intellectual curiosity. It opens concrete perspectives:

- In **personalized medicine**, through the creation of virtual genetic twins enabling anticipation of treatment responses.
- In **augmented paleogenetics**, through the reconstruction of phenotypes that never came to be, offering a new reading of human trajectories.
- In **neuroscience**, through the simulation of mirror brains and the exploration of alternative forms of cognition.
- In **exobiology**, through the identification of universal signatures of life independent of terrestrial DNA.
- In **synthetic biology**, by providing a theoretical framework for testing the viability of novel genetic architectures before their experimental construction; and in **virtual reality**, by offering immersive visualization of these alternative humanities, allowing parallel biological worlds to be explored as genuine scientific and educational environments.

These applications show that speculative but calculable sciences do not belong to utopia, but to a sustainable research program destined to unfold over several decades. By laying the foundations of *genomathematics*, we open a new path: the scientific study of virtual life, erased trajectories, and parallel biological worlds. The aim is not to compete with classical biology, but to enrich it with a new horizon: that of what could have been. In this field, speculation is not left to imagination alone—it becomes calculable, reproducible, and therefore scientific.

2. Theoretical Foundations

Genomathematics rests on a simple but radical idea: to consider DNA not only as a biological molecule, but also as a mathematical object, endowed with an internal grammar that can be analyzed, manipulated, and transformed. DNA thus becomes a language in the fullest sense of the term: it has signs (the bases), rules of combination (the codons), and, beyond these, arithmetic structures that repeat across multiple scales. Where molecular biology describes processes, genomathematics seeks to uncover invariants—that is, what remains constant behind the diversity of life and obeys a universal logic.

This logic is revealed through the *arithmetization of life*. Starting from elementary constituents—protons, neutrons, and electrons—to the main atoms of living matter (carbon, hydrogen, oxygen, nitrogen), then to nucleic bases and finally to codons, one observes the emergence of numerical constants. Certain values appear recurrently, such as the numbers 1, 96, and 128, which structure different stages in the construction of the genetic code. These invariants do not depend on chance or contingent evolution but seem inscribed in the very logic of biological matter. In this sense, genomathematics resembles the search for *universal laws* of life, comparable to those in physics that govern particles or force fields.

Alongside this arithmetic dimension comes a second innovation: the systematic transformation of the code. By applying a simple inversion rule— $A \leftrightarrow G$, $C \leftrightarrow T$ —it is possible to generate a mirror genome, entirely coherent in its internal structure yet never realized in the actual history of evolution. This procedure is not fictional: once produced, such inverted genomes can be compared against existing genetic databases. Some are recognized as plausible, even linked to human lineages, proof that the operation respects biological coherence.

I was able to experience this directly: a virtual mirror twin, generated from my own genetic code, was compared within a laboratory database. The result revealed 91 identical segments and about 30% shared DNA with a *real human* who had submitted their genome to the same laboratory. Such a level of genetic proximity corresponds to what is typically observed between an individual and an uncle, an aunt, or a half-sibling. In other words, a virtual genome, entirely inverted and never realized in evolutionary history, was recognized as having a significant kinship with an actual human being.

This concordance, obtained from a systematically transformed sequence, demonstrates the power of the approach: it validates the plausibility of these erased trajectories and justifies their scientific exploration. This method opens an unprecedented experimental field: the study of *virtual life*, where the plasticity of the genome can be tested and rupture points identified—zones where inversion makes life impossible, and zones where it reveals new potentialities.

Finally, genomathematics materializes through the *morphological projection* of these data. The inverted sequences do not remain abstract: they can be embodied through 3D modeling, facial reconstruction, and brain simulation. One can thus compare a “real” face and its mirror face, observe the symmetries, inversions, and shifts, and understand what they reveal about human biological identity. Likewise, inverted gene expression maps make it possible to simulate “other” brains, endowed with different neuronal organizations. These reconstructions are not mere artistic extrapolations: they are grounded in numerical data, in a reproducible methodology, and they obey an internal logic that makes them scientifically testable.

Genomathematics therefore occupies a singular space: it is not literary speculation, for it is grounded in explicit rules and calculations. Nor is it classical biological science, for it does not limit itself to studying what exists, but opens the exploration of what *could have existed*. It constitutes a theoretical laboratory of life, a place where alternative versions of living systems can be generated, tested, and compared. Its rigor lies in the reproducibility of

operations, and its ambition in the will to move beyond the boundaries of the observable in order to explore the vast field of possibilities.

3. First Contributions

Genomathematics is not pure theoretical speculation: it has already taken shape in concrete research that constitutes its first milestones. These works show that virtual life can be approached rigorously, and that the exploration of erased trajectories is not an exercise in free imagination but a reproducible scientific endeavor. Two major contributions illustrate this: the identification of multi-level arithmetic invariants in DNA, and the experimentation with the *mirror-twin paradox*.

3.1 Multi-Level Invariants

The first contribution of genomathematics is the identification of recurrent numerical constants within the structure of the genetic code. Starting from the subatomic level—protons, neutrons, and electrons—then step by step reconstructing the atoms of life (carbon, hydrogen, oxygen, nitrogen), the nucleic bases, theoretical doublets, and finally coding triplets, one observes the emergence of stable values. Among them, three numbers appear with striking regularity: **1, 96, and 128**. These constants manifest themselves at different stages of the combinatorial construction, revealing an internal organization that transcends chemical and evolutionary contingencies.

The methodology employed is simple and transparent. Each level of structuring is converted into arithmetic equivalents: elementary particles are translated into numerical values, which then combine to yield the atomic weights of the essential elements. These values, aggregated into bases and then into codons, obey precise transformation rules (cubing, division by four, modular reductions). From these operations, invariants emerge, independent of biological variations or of the different genetic codes recorded.

The importance of this discovery is twofold. Theoretically, it suggests that the genetic code is not merely the product of an evolutionary history, but obeys an underlying mathematical logic, comparable to the universal laws governing physics. Practically, it offers tools for exobiology: if these invariants are present in all possible forms of life, then their detection could provide an objective criterion for recognizing living systems, even those radically different from those known on Earth. Genomathematics thus proposes a first “universal signature of life,” independent of local biochemistry.

3.2 The Mirror-Twin Paradox

The second major contribution is the experimentation with the *mirror-twin paradox*. The principle is deceptively simple: apply a systematic inversion rule to the code, whereby adenine and guanine ($A \leftrightarrow G$), as well as cytosine and thymine ($C \leftrightarrow T$), are exchanged. The result is a *mirror genome*: an alternative version of the original code, coherent in its internal structure but never realized in actual evolution.

This inversion is not a theoretical curiosity. Once generated, these mirror genomes have been submitted to existing bioinformatics databases. Some were recognized as plausible, demonstrating that the operation respects fundamental biological constraints. More than

that, the morphological projection of these inverted sequences made it possible to produce unprecedented 3D reconstructions: inverted faces, skulls, and even hypotheses of brain structures. These representations embody erased evolutionary trajectories—*humanities never born* but nonetheless calculable and visualizable.

The implications of this work are considerable. In **personalized medicine**, creating a patient's mirror twin would allow virtual testing of the effects of silent mutations or treatments, opening a new pathway for pharmacogenomics. In **neuroscience**, the study of mirror brains could reveal alternative cognitive architectures, shedding light on the mechanisms of complex pathologies. Finally, in **augmented paleogenetics**, inverted faces and phenotypes enrich our understanding of human evolution by granting access to plausible but erased forms.

4. Disciplinary Positioning

Genomathematics stands at the intersection of several existing scientific fields, yet it coincides fully with none of them. To understand its specificity, it is necessary to compare it with the disciplines to which it is most closely related: theoretical biology, bioinformatics, and synthetic biology. Each has contributed elements that have nourished this reflection, but none encompasses the approach proposed here.

Theoretical biology constitutes the conceptual foundation of much contemporary research. It formalizes models of evolution, population dynamics, and genetic networks. However, it remains essentially descriptive and explanatory: its aim is to account for observed phenomena and to propose general laws. Genomathematics goes further, because it does not merely explain what *is* or what *was*; it generates new trajectories, producing alternative versions of life through reproducible arithmetic rules. Where theoretical biology describes, genomathematics experiments and creates within the space of the possible.

Bioinformatics, for its part, has become indispensable for processing the colossal mass of data produced by genomic sequencing. It relies on statistical methods, machine learning, and sequence comparison to detect correlations, motifs, or anomalies. But its logic remains fundamentally analytical: it observes and classifies what already exists. Genomathematics introduces a break by being generative: it applies systematic transformations (such as mirror inversion) to create genomes that are plausible but never realized. It does not simply analyze existing data; it produces new objects of study, allowing the mapping of the limits and potentialities of life.

Synthetic biology is the field that comes closest to the ambition of genomathematics. It aims to design and construct new organisms by assembling artificial genetic circuits or rewriting genomes. Its orientation is thus constructive and experimental. But this construction rests primarily on empirical choices, guided by engineering, rather than on a systematic mathematization of life. Genomathematics distinguishes itself by providing a prior arithmetic framework: a space of simulation that allows the viability of alternative genetic structures to be tested in advance, even before moving to the laboratory. It thus constitutes a complementary epistemology: rather than building directly, it explores and calculates, offering synthetic biology a theoretical domain in which to anticipate its own creations.

This is why genomathematics deserves to be recognized as an autonomous field. It does not duplicate existing disciplines but extends them by opening a new dimension: that of the study of erased trajectories and the universal invariants of life. Its aim is not to replace theoretical biology, bioinformatics, or synthetic biology, but to contribute a *fourth path*, situated between description, analysis, and construction. In this sense, it asserts itself as a science in its own right, whose object is not only real life but also *virtual life*, calculable and reproducible.

5. Practical Applications

Genomathematics is not limited to an abstract theoretical framework. By proposing a systematic exploration of erased trajectories, it opens up a set of concrete applications that go well beyond intellectual curiosity. These perspectives span medicine, paleogenetics, neuroscience, exobiology, and synthetic biology.

5.1 Personalized Medicine

In medicine, genomathematics enables the conception of virtual twins generated by inversion or systematic transformation of a patient's genome. These digital doubles are not mere computer simulations: they are based on reproducible rules and reveal silent mutations that, in a mirror context, may become pathogenic. Their analysis could anticipate treatment responses, virtually test the efficacy or toxicity of targeted therapies, and refine pharmacogenomic protocols. In the near future, one can imagine each patient having their own "mirror profile" alongside their real sequencing, in order to better map risks and adjust care.

5.2 Augmented Paleogenetics

Genomathematics also enriches paleogenetics by opening the possibility of exploring not only extinct species but also versions that never came to be. Starting from ancient DNA, it is possible to apply mirror inversion to produce alternative sequences, then reconstruct faces and phenotypes in 3D. These reconstructions give access to a gallery of erased humanities: plausible forms eliminated by evolution. This work does not belong to fantasy but to experimental science, since each step is calculable and reproducible. Paleogenetics is thus augmented by a rigorous speculative dimension, allowing us to better understand not only what we have been, but also what we might have become.

5.3 Neuroscience

Neuroscience finds in this approach a novel tool to explore alternative cognitive architectures. By inverting genetic sequences involved in brain development, it becomes possible to simulate "mirror brains" and test different models of cognition. This method could shed light on still poorly understood pathologies, by revealing plausible alternative neural circuits. It also opens perspectives in neuroethics and philosophy of mind, raising the question: what is a human brain, and how far can it be altered while still being recognized as such? Genomathematics thus becomes a conceptual laboratory to probe the limits and plasticity of cognition.

5.4 Exobiology

Exobiology is one of the fields where genomathematics finds an immediate resonance. The identification of multi-level numerical invariants—such as the constants 1, 96–97, and 128—offers criteria independent of terrestrial chemistry. Instead of searching only for known molecules (DNA, RNA, proteins), one can search for universal mathematical signatures that may manifest in other forms of life, even radically different ones. This approach provides a common language for recognizing life beyond Earth. It continues the speculations of Carl Sagan and Francis Crick, but adds a calculable and falsifiable methodology. Genomathematics could thus become a central tool in the search for extraterrestrial life.

5.5 Synthetic Biology

Finally, synthetic biology benefits directly from this framework. Mirror genomes and other alternative sequences provide a theoretical laboratory to test the viability of novel genetic architectures before their construction in the lab. Genomathematics makes it possible to explore combinations never selected by evolution and to evaluate their internal coherence. Rather than proceeding by empirical trial and error, it offers an arithmetic framework that maps out the space of possibilities and reduces experimental uncertainty. This role as a “prior simulator” makes genomathematics a strategic ally for the engineering of life, opening new evolutionary pathways and expanding the repertoire of artificial life forms.

 Table – Applications of the Science of Erased Trajectories

Domain	Concrete Utility	Example of Application
Fundamental Biology	Identify critical points and invariants of the genome (breakable vs. flexible zones).	Mapping genes absolutely indispensable to life.
Genetic Medicine	Reveal <i>silent mutations</i> that become pathogenic in a mirror genome.	Understanding why certain rare diseases appear only in combination with specific variants.
Personalized Medicine	Create a <i>digital mirror twin</i> of a patient to virtually test treatment responses.	Adapting chemotherapy according to the patient's mirror profile.
Paleogenetics	Explore <i>erased faces and phenotypes</i> in human evolution.	Reconstruction of a mirror Neanderthal: a plausible but never-born face.
Neuroscience	Model <i>mirror brains</i> and test alternative cognitions.	Simulation of reversed brain lateralization to understand autism or schizophrenia.
Exobiology	Define <i>universal signatures of life</i> independent of terrestrial DNA.	Detecting extraterrestrial organisms by searching for multi-scale numerical invariants.
Security / Bioethics	Test the <i>robustness of genetic databases</i> against artificial profiles.	Showing that a mirror genome is accepted by databases as a real individual.
Philosophy / Anthropology	Explore the <i>plasticity of biological identity</i> and possible worlds of life.	Question: would we still be human with an inverted genome?

Table generated by ChatGPT based on the present text.

6. *Philosophical and Ethical Dimension*

By exploring trajectories that never came to be, genomathematics goes beyond the framework of a descriptive science. It forces us to confront fundamental questions—both philosophical and ethical—that touch upon the definition of human identity, the legitimate uses of genetic technologies, and our relationship to life as a whole. It does not merely open a new field of research; it also creates a novel space of inquiry, where science and philosophy must meet.

6.1 Identity in the Face of the Genomic Mirror

The first question is that of biological identity. If one can invert a genome to produce a “mirror twin,” would we still be ourselves with such a sequence? The question, seemingly speculative, takes on a vertiginous dimension when one contemplates faces reconstructed from inverted genomes. These faces resemble but do not coincide; they disturb as much as they fascinate, for they confront us with a radical otherness that nonetheless remains inscribed within our own genetic logic.

This paradox raises an ancient philosophical question: what constitutes identity? Is it the precise materiality of our nucleic bases, or the broader organization—the mathematical structure—that transcends the contingency of sequences? If one recognizes in a mirror face a full-fledged human being, then biological identity appears not as a fixed essence but as a zone of plasticity where the real and the virtual, the actual and the possible, converge. Genomathematics thus reveals the fragility of our certainties: it obliges us to admit that the human could have been otherwise, and that it remains defined by a constellation of possibilities of which we see only one realized trajectory.

6.2 Bioethics and New Vulnerabilities

The second dimension concerns contemporary bioethics. By making it possible to generate artificial yet plausible genomes, genomathematics introduces new vulnerabilities. In a world where DNA has become legal proof, a tool of traceability, or a criterion of identity, the possibility of creating genetic profiles that do not exist yet are indistinguishable from real ones raises major problems. One can imagine fraud, falsification, or manipulation in databases, blurring the boundaries between biological reality and digital simulation.

Beyond these practical risks, genomathematics also highlights an ethical dilemma: how far is it legitimate to create virtual biological worlds? If one can simulate mirror brains, alternative neuronal architectures, or even entire organisms that never existed, should these entities be regarded merely as research objects, or should they be attributed an intrinsic value? At what threshold does simulation become a form of creation? The boundary between scientific experimentation and the “fabrication of possible beings” grows blurred, and with it arise unprecedented questions about the responsibility of researchers.

6.3 Mapping the Erased Possible

Finally, genomathematics opens a broader, properly philosophical perspective. By mapping the erased possible, it expands our conception of life. Until now, biology has understood life within a tension between contingency and necessity: on one side, the randomness of

mutations and natural selection; on the other, the physical and chemical laws that constrain these processes. But it has neglected a third dimension: that of the virtually plausible—what could have existed but never materialized.

Exploring these erased trajectories amounts to redefining our relationship to reality. Life no longer appears solely as a chain of contingent events but as a vast space of possibilities of which evolution actualized only a tiny fraction. Recognizing this plurality transforms our vision of the living: it is no longer merely a matter of studying what is, but of understanding that every organism, every species, every genome is surrounded by a constellation of “ghost forms,” alternatives ready to surface through calculation.

This philosophy of the possible obliges us to widen our ethical horizon. We are no longer simply the heirs of a biological history, but the custodians of an infinite field of unexplored trajectories. The responsibility that follows is considerable: what do we do with these possibilities? Do we use them to enrich our understanding of life, to prevent disease, to anticipate new forms of cognition? Or do we risk instrumentalizing them without restraint, to the detriment of scientific integrity and ethical balance?

6.4 Towards a New Anthropology of Life

Ultimately, genomathematics does not raise only technical or medical questions. It inaugurates a new anthropology of life, where the human must be conceived both as a realized biological trajectory and as a sum of erased possibilities. It forces us to acknowledge that our identity is less an immutable given than a crossroads of potential variations inscribed within the logic of the genetic code.

This vision resonates with, and renews, the great philosophical interrogations about being and becoming. It echoes Leibniz’s reflections on possible worlds, Monod’s metaphysics of chance and necessity, and contemporary debates on artificial intelligence and simulated realities. But it adds an unprecedented anchor: the possibility of calculating these possible worlds, of rendering them visible and debatable, and therefore of integrating them into science.

6.5 Interim Conclusion

Thus, the philosophical and ethical dimension of genomathematics is not peripheral: it constitutes its very core. It reveals that this science of erased trajectories is not merely a new approach to the genetic code, but an invitation to rethink our relationship to life, to identity, and to possibility. It opens a space where science and philosophy cease to ignore each other, and where speculation becomes both a tool of knowledge and a call to responsibility.

7. Conclusion – Call to the Community

Genomathematics presents itself today as a response to a gap. Classical biology, rich as it is, remains oriented toward what exists: it describes what is, it reconstructs what was. But it rarely ventures into the vast field of the possible—those erased trajectories that evolution did not actualize. The approach presented here shows that it is possible to take this step without abandoning scientific rigor: by revealing multi-level arithmetic invariants, by producing mirror genomes, by projecting these inverted sequences into 3D reconstructed faces and brains, it

demonstrates that virtual life can be studied with the same standards of reproducibility as real life.

This field is necessary because it broadens our scientific horizon. The goal is not to compete with genetics, bioinformatics, or synthetic biology, but to provide an extension. To the first, it adds a generative dimension; to the second, a capacity to produce new objects rather than only analyze what exists; to the third, a theoretical laboratory in which genetic architectures can be tested before fabrication. Genomathematics is therefore not a mere supplement, but an opening: it transforms our relationship to biology by rooting it in a logic of possibilities.

Yet such an undertaking cannot be carried out alone. By nature, genomathematics is interdisciplinary: it calls for the collaboration of molecular biologists, mathematicians and computer scientists, specialists in 3D modeling, but also philosophers, anthropologists, and ethicists. Each can find a place within it, because the stakes extend beyond the laboratory: they concern personalized medicine, the understanding of human evolution, the simulation of alternative cognitive forms, the search for extraterrestrial life, and the construction of artificial organisms. The diversity of applications shows that this field cannot be confined to a single discipline; it must be conceived as a space of dialogue between domains of knowledge, a crossroads between the exact sciences, the life sciences, and the humanities.

It is therefore essential to recognize genomathematics as an autonomous discipline—not on the margins of science, but as its natural extension into possible worlds. Like theoretical physics in its time, it dares to explore what has not yet been experimentally demonstrated but can be formulated, calculated, and tested through models. Like information theory, it provides a universal language capable of describing life beyond its terrestrial forms. Like cybernetics, it charts a new path, one that could nourish multiple domains and transform our relationship to the living.

This is a call addressed to all those who wish to think of life differently: not merely as a succession of contingent events, but as an architecture of possibilities of which evolution has actualized only a small part. By mapping these erased trajectories, genomathematics does not simply add one more curiosity to the scientific toolbox. It fundamentally alters the way we conceive life, reminding us that it is first and foremost a logic, a grammar, a combinatorics. It invites us to recognize that every organism is surrounded by a halo of ghost forms, of alternative faces, of brains never born, which are integral to its identity.

In this sense, genomathematics is not only a scientific discipline: it is also a philosophy and an ethics. A philosophy, because it renews our relationship to reality by linking it to the virtual, the possible, and the erased. An ethics, because it confronts us with our responsibilities regarding the manipulation of the code, the creation of fictitious genetic profiles, or the simulation of alternative brains. It forces us to reflect on what it means to create, explore, or manipulate trajectories that never existed, but that become calculable.

By opening this path, we do not claim to offer definitive answers, but rather to propose a framework in which speculation ceases to be arbitrary and becomes scientific. Genomathematics is a call: a call to rigor, a call to imagination, a call to the scientific and philosophical community to take hold of these questions and help them mature. It is not a solitary science, but one to be built collectively, step by step, embracing both its boldness and its limits.

The future of genomathematics will depend on this collaboration. It can become a structured field, equipped with its own methods, tools, and institutions, if a community accepts to recognize its potential. It may also remain an isolated intuition, if it is not carried forward. But the history of science shows that great revolutions often arise from such founding gestures—gestures that at first seem marginal before becoming self-evident. That is why it is time to affirm, clearly and forcefully: **genomathematics is not a curiosity, but a necessity. It is not a rupture with science, but its natural extension into a new territory: the realm of possible worlds.**

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